



Attachment
9/c

SEQUENCE LISTING

<110> WUCHERPENNIG, Kai W
STROMINGER, Jack L

<120> MONOVALENT, MULTIVALENT AND MULTIMERIC MHC BINDING DOMAIN FUSION PROTEINS AND CONJUGATES, AND USES THEREFOR

<130> HAR-005

<140> 09/248,964

<141> 1999-02-12

<150> PCT/US97/14503

<151> 1997-08-15

<150> 60/075,351

<151> 1998-02-19

<150> 60/024,007

<151> 1996-08-15

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 750

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DR2-Fos fusion

<220>

<221> CDS

<222> (1)..(735)

<220>

<221> misc_feature

<222> (1)..(21)

<223> 3' end of secretory signal

<220>

<221> misc_structure

<222> (22)..(594)

<223> DRA*0101 extracellular domain

<220>

<221> misc_feature

<222> (595)..(615)

<223> Linker sequence

<220>

<221> misc_feature

<222> (616)..(735)





<223> Fos leucine zipper domain

<400> 1

gta tct ctc gag aaa aga gag atc aaa gaa gaa cat gtg atc atc cag 48
 Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln
 1 5 10 15

gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac 96
 Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp
 20 25 30

ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg 144
 Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
 35 40 45

gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa 192
 Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
 50 55 60

ggg gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg 240
 Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met
 65 70 75 80

aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta 288
 Thr Lys Arg Ser Asn Tyr Thr Pro Ile Asn Val Pro Pro Glu Val
 85 90 95

act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc 336
 Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu
 100 105 110

atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg 384
 Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp
 115 120 125

ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc 432
 Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe
 130 135 140

ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc 480
 Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe
 145 150 155 160

ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc 528
 Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly
 165 170 175

ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct 576
 Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro
 180 185 190

ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat 624
 Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Leu Thr Asp
 195 200 205

aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg 672
 Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu

RECEIVED

JUL 31 2000

TECH CENTER 1600/2900

RECEIVED

JUL 28 2000

TECH CENTER 1600/2900



210

215

220

cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc 720
Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
225 230 235 240

atc ctg gcc gcc cat tgagaattct atgac 750
Ile Leu Ala Ala His
245

<210> 2
<211> 245
<212> PRT
<213> Artificial Sequence

<400> 2
Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln
1 5 10 15

Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp
20 25 30

Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
35 40 45

Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
50 55 60

Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met
65 70 75 80

Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val
85 90 95

Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu
100 105 110

Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp
115 120 125

Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe
130 135 140

Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe
145 150 155 160

Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly
165 170 175

Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro
180 185 190

Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Leu Thr Asp
195 200 205

Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu



210

215

220

Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
225 230 235 240

Ile Leu Ala Ala His
245

<210> 3
<211> 771
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DR@-Jun fusion

<220>
<221> CDS
<222> (1)..(756)

<220>
<221> misc_feature
<222> (1)..(21)
<223> 3' end of secretory signal

<220>
<221> misc_feature
<222> (22)..(615)
<223> DRB1*1501 extracellular domain

<220>
<221> misc_feature
<222> (616)..(636)
<223> Linker sequence

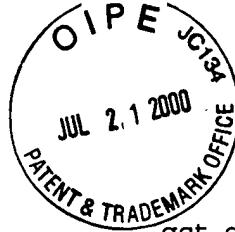
<220>
<221> misc_feature
<222> (637)..(756)
<223> Jun leucine zipper domain

<400> 3
gta tct ctc gag aaa aga gag ggg gac acc cga cca cgt ttc ctg tgg 48
Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp
1 5 10 15

cag cct aag agg gag tgt cat ttc ttc aat ggg acg gag cgg gtg cgg 96
Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
20 25 30

ttc ctg gac aga tac ttc tat aac cag gag tcc gtg cgc ttc gac 144
Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Ser Val Arg Phe Asp
35 40 45

agc gac gtg ggg gag ttc cgg gcg gtg acg gag ctg ggg cgg cct gac 192
Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
50 55 60



gct gag tac tgg aac agc cag aag gac atc ctg gag cag gcg cg	240
Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala	
65 70 75 80	
gcg gtg gac acc tac tgc aga cac aac tac ggg gtt gtg gag agc ttc	288
Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe	
85 90 95	
aca gtg cag cg cg a gtc caa cct aag gtg act gta tat cct tca aag	336
Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys	
100 105 110	
acc cag ccc ctg cag cac aac ctc ctg gtc tgc tct gtg agt ggt	384
Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly	
115 120 125	
ttc tat cca ggc agc att gaa gtc agg tgg ttc ctg aac ggc cag gaa	432
Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu	
130 135 140	
gag aag gct ggg atg gtg tcc aca ggc ctg atc cag aat gga gac tgg	480
Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp	
145 150 155 160	
acc ttc cag acc ctg gtg atg ctg gaa aca gtt cct cga agt gga gag	528
Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu	
165 170 175	
gtt tac acc tgc caa gtg gag cac cca agc gtg aca agc cct ctc aca	576
Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr	
180 185 190	
gtg gaa tgg aga gca cgg tct gaa tct gca cag agc aag gtc gac gga	624
Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly	
195 200 205	
ggt ggc ggc ggt cgc atc gcc cgg ctc gag gaa aaa gtg aaa acc ttg	672
Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu	
210 215 220	
aaa gct cag aac tcg gag ctc gcg tcc acg gcc aac atg ctc agg gaa	720
Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu	
225 230 235 240	
cag gtg gca cag ctt aaa cag aaa gtc atg aac cat tgagaattct atgac	771
Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His	
245 250	

<210> 4
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<400> 4
 Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp



5

10

15

Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
20 25 30

Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp
35 40 45

Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
50 55 60

Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala
65 70 75 80

Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
85 90 95

Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
100 105 110

Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly
115 120 125

Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
130 135 140

Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
145 150 155 160

Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
165 170 175

Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
180 185 190

Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
195 200 205

Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
210 215 220

Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
225 230 235 240

Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His
245 250

<210> 5

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR
primer



<400> 5

gtatctctcg agaaaaagaga gatcaaagaa gaacatgtga tc

42

<210> 6

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 6

gtcatagaat tctcaatggg cggccaggat gaactccag

39

<210> 7

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 7

gtatctctcg agaaaaagaga gggggacacc cgaccacgtt tc

42

<210> 8

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 8

gtcatagaat tctcaatggt tcatgacttt ctgtttaag

39

<210> 9

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic, biotin ligase recognition sequence

<400> 9

Leu Gly Gly Ile Phe Glu Ala Met Lys Met Glu Leu Arg Asp

1

5

10



<210> 10
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic,
linker sequence

<400> 10
Ser Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 11
<211> 1446
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DR2-IgG fusion

<220>
<221> CDS
<222> (1)..(1437)

<220>
<221> misc_feature
<222> (1)..(15)
<223> 3' end of secretory signal

<220>
<221> misc_feature
<222> (16)..(588)
<223> DRA*0101 extracellular domain

<220>
<221> misc_feature
<222> (589)..(609)
<223> Linker

<220>
<221> misc_feature
<222> (610)..(729)
<223> Fos leucine zipper domain

<220>
<221> misc_feature
<222> (730)..(1437)
<223> IgG domain

<400> 11
ctc gag aaa aga gag atc aaa gaa gaa cat gtg atc atc cag gcc gag 48
Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu
1 5 10 15

ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac ttt gat 96



Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Met Phe Asp Phe Asp
20 25 30

ggg gat gag att ttc cat gtg gat atg gca aag aag gag acg gtc tgg 144
Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
35 40 45

cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa ggt gca 192
Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
50 55 60

ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg aca aag 240
Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
65 70 75 80

cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta act gtg 288
Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val
85 90 95

ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc atc tgt 336
Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys
100 105 110

ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg ctt cga 384
Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg
115 120 125

aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc ctg ccc 432
Asn Gly Lys Pro Val Thr Gly Val Ser Glu Thr Val Phe Leu Pro
130 135 140

agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc ctg ccc 480
Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro
145 150 155 160

tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc ttg gat 528
Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp
165 170 175

gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct ctc cca 576
Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro
180 185 190

gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat aca ctc 624
Glu Thr Thr Glu Val Asp Gly Gly Gly Leu Thr Asp Thr Leu
195 200 205

caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg cag acc 672
Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln Thr
210 215 220

gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc atc ctg 720
Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu
225 230 235 240

gcc gcc cat gca gca tct gag ccc aga ggg ccc aca atc aag ccc tgt 768
Ala Ala His Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys



245

250

255

cct cca tgc aaa tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc 816
 Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
 260 265 270

ttc atc ttc cct cca aag atc aag gat gta ctc atg atc tcc ctg agc 864
 Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
 275 280 285

ccc ata gtc aca tgt gtg gtg gat gtg agc gag gat gac cca gat 912
 Pro Ile Val Thr Cys Val Val Asp Val Ser Glu Asp Asp Pro Asp
 290 295 300

gtc cag atc agc tgg ttt gtg aac aac gtg gaa gta cac aca gct cag 960
 Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
 305 310 315 320

aca caa acc cat aga gag gat tac aac agt act ctc cgg gtg gtc agt 1008
 Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
 325 330 335

gcc ctc ccc atc cag cac cag gac tgg atg agt ggc aag gag ttc aaa 1056
 Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
 340 345 350

tgc aag gtc aac aac aaa gac ctc cca gcg ccc atc gag aga acc atc 1104
 Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
 355 360 365

tca aaa ccc aaa ggg tca gta aga gct cca cag gta tat gtc ttg cct 1152
 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
 370 375 380

cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc tgc atg 1200
 Pro Pro Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
 385 390 395 400

gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc aac aac 1248
 Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
 405 410 415

ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg gac tct 1296
 Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
 420 425 430

gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag aag aac 1344
 Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
 435 440 445

tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg 1392
 Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
 450 455 460

cac aat cac cac acg act aag agc ttc tcc cgg act ccg ggt aaa 1437
 His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
 465 470 475



tgagaattc

1446

<210> 12
<211> 479
<212> PRT
<213> Artificial Sequence

<400> 12
Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu
1 5 10 15

Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp
20 25 30

Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
35 40 45

Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
50 55 60

Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
65 70 75 80

Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val
85 90 95

Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys
100 105 110

Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg
115 120 125

Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro
130 135 140

Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro
145 150 155 160

Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp
165 170 175

Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro
180 185 190

Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Leu Thr Asp Thr Leu
195 200 205

Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln Thr
210 215 220

Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu
225 230 235 240

Ala Ala His Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
245 250 255



Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
260 265 270

Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
275 280 285

Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
290 295 300

Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
305 310 315 320

Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
325 330 335

Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
340 345 350

Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
355 360 365

Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
370 375 380

Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
385 390 395 400

Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
405 410 415

Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
420 425 430

Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
435 440 445

Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
450 455 460

His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
465 470 475

<210> 13
<211> 1851
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DR2-IgM fusion

<220>
<221> CDS
<222> (1)..(1836)

<220>



<221> misc_feature
<222> (1)..(75)
<223> 3' end of secretory signal

<220>
<221> misc_feature
<222> (76)..(648)
<223> DRA*0101 extracellular domain

<220>
<221> misc_feature
<222> (649)..(669)
<223> Linker

<220>
<221> misc_feature
<222> (670)..(789)
<223> Fos leucine zipper domain

<220>
<221> misc_feature
<222> (790)..(1836)
<223> IgG domain

<400> 13

atg	gcc	ata	agt	gga	gtc	cct	gtg	cta	gga	ttt	ttc	atc	ata	gct	gtg	48
Met	Ala	Ile	Ser	Gly	Val	Pro	Val	Leu	Gly	Phe	Phe	Ile	Ile	Ala	Val	
1		5						10				15				

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc 96

Leu	Met	Ser	Ala	Gln	Glu	Ser	Trp	Ala	Ile	Lys	Glu	Glu	His	Val	Ile	
20								25				30				

atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg 144

Ile	Gln	Ala	Glu	Phe	Tyr	Leu	Asn	Pro	Asp	Gln	Ser	Gly	Glu	Phe	Met	
35								40				45				

ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag 192

Phe	Asp	Phe	Asp	Gly	Asp	Glu	Ile	Phe	His	Val	Asp	Met	Ala	Lys	Lys	
50							55		60							

gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag 240

Glu	Thr	Val	Trp	Arg	Leu	Glu	Phe	Gly	Arg	Phe	Ala	Ser	Phe	Glu		
65							70		75			80				

gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa 288

Ala	Gln	Gly	Ala	Leu	Ala	Asn	Ile	Ala	Val	Asp	Lys	Ala	Asn	Leu	Glu	
85								90				95				

atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca 336

Ile	Met	Thr	Lys	Arg	Ser	Asn	Tyr	Thr	Pro	Ile	Thr	Asn	Val	Pro	Pro	
100								105			110					

gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac 384

Glu	Val	Thr	Val	Leu	Thr	Asn	Ser	Pro	Val	Glu	Leu	Arg	Glu	Pro	Asn	
115								120			125					



cc ctc atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc	432
Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val	
130 135 140	
acg tgg ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca	480
Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr	
145 150 155 160	
gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc	528
Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu	
165 170 175	
ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac	576
Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His	
180 185 190	
tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca	624
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro	
195 200 205	
agc cct ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta	672
Ser Pro Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Leu	
210 215 220	
act gat aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct	720
Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser	
225 230 235 240	
gcg ttg cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg	768
Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu	
245 250 255	
gag ttc atc ctg gcc gcc cac gtc gca gaa atg aac ccc aat gta aat	816
Glu Phe Ile Leu Ala Ala His Val Ala Glu Met Asn Pro Asn Val Asn	
260 265 270	
gtg ttc gtc cca cca cgg gat ggc ttc tct ggc cct gca cca cgc aag	864
Val Phe Val Pro Pro Arg Asp Gly Phe Ser Gly Pro Ala Pro Arg Lys	
275 280 285	
tct aaa ctc atc tgc gag gcc acg aac ttc act cca aaa ccg atc aca	912
Ser Lys Leu Ile Cys Glu Ala Thr Asn Phe Thr Pro Lys Pro Ile Thr	
290 295 300	
gta tcc tgg cta aag gat ggg aag ctc gtg gaa tct ggc ttc acc aca	960
Val Ser Trp Leu Lys Asp Gly Lys Leu Val Glu Ser Gly Phe Thr Thr	
305 310 315 320	
gat ccg gtg acc atc gag aac aaa gga tcc aca ccc caa acc tac aag	1008
Asp Pro Val Thr Ile Glu Asn Lys Gly Ser Thr Pro Gln Thr Tyr Lys	
325 330 335	
gtc ata agc aca ctt acc atc tct gaa atc gac tgg ctg aac ctg aat	1056
Val Ile Ser Thr Leu Thr Ile Ser Glu Ile Asp Trp Leu Asn Leu Asn	
340 345 350	
gtg tac acc tgc cgt gtg gat cac agg ggt ctc acc ttc ttg aag aac	1104



Val Tyr Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Leu Lys Asn			
355	360	365	
gtg tcc tcc aca tgt gct gcc agt ccc tcc aca gat atc ctt aat ttt			1152
Val Ser Ser Thr Cys Ala Ala Ser Pro Ser Thr Asp Ile Leu Asn Phe			
370	375	380	
act att cct cct tcc ttt gcc gac atc ttc ctt agc aag tcc gct aac			1200
Thr Ile Pro Pro Ser Phe Ala Asp Ile Phe Leu Ser Lys Ser Ala Asn			
385	390	395	400
ctg acc tgt ctg gtc tca aac ctg gca acc tat gaa acc ctg agt atc			1248
Leu Thr Cys Leu Val Ser Asn Leu Ala Thr Tyr Glu Thr Leu Ser Ile			
405	410	415	
tcc tgg gct tct caa agt ggt gaa cca ctg gaa acc aaa att aaa atc			1296
Ser Trp Ala Ser Gln Ser Gly Glu Pro Leu Glu Thr Lys Ile Lys Ile			
420	425	430	
atg gaa agc cat ccc aat ggc acc ttc agt gct aag ggt gtg gct agt			1344
Met Glu Ser His Pro Asn Gly Thr Phe Ser Ala Lys Gly Val Ala Ser			
435	440	445	
gtt tgt gtg gaa gac tgg aat aac agg aag gaa ttt gtg tgt act gtg			1392
Val Cys Val Glu Asp Trp Asn Asn Arg Lys Glu Phe Val Cys Thr Val			
450	455	460	
act cac agg gat ctg cct tca cca cag aag aaa ttc atc tca aaa ccc			1440
Thr His Arg Asp Leu Pro Ser Pro Gln Lys Lys Phe Ile Ser Lys Pro			
465	470	475	480
aat gag gtg cac aaa cat cca cct gct gtg tac ctg ctg cca cca gct			1488
Asn Glu Val His Lys His Pro Pro Ala Val Tyr Leu Leu Pro Pro Ala			
485	490	495	
cgt gaa caa ctg aac ctg agg gag tca gcc aca gtc acc tgc ctg gtg			1536
Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Val Thr Cys Leu Val			
500	505	510	
aag ggc ttc tct cct gca gac atc tct gtg caa tgg aag cag agg ggc			1584
Lys Gly Phe Ser Pro Ala Asp Ile Ser Val Gln Trp Lys Gln Arg Gly			
515	520	525	
cag ctc tta ccc cag gag aag tat gtg acc agt gcc ccg atg cca gag			1632
Gln Leu Leu Pro Gln Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu			
530	535	540	
cct ggg gcc cca ggc ttc tac ttt acc cac agc atc ctg act gtg aca			1680
Pro Gly Ala Pro Gly Phe Tyr Phe Thr His Ser Ile Leu Thr Val Thr			
545	550	555	560
gag gag gaa tgg aac tcc gga gag acc tat acc tgt gtt gta ggc cac			1728
Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr Thr Cys Val Val Gly His			
565	570	575	
gag gcc ctg cca cac ctg gtg acc gag agg acc gtg gac aag tcc act			1776
Glu Ala Leu Pro His Leu Val Thr Glu Arg Thr Val Asp Lys Ser Thr			



580

585

590

ggt aaa ccc aca ctg tac aat gtc tcc ctg atc atg tct gac aca ggc
 Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly
 595 600 605

1824

ggc acc tgc tat tgaagatctg tcgac
 Gly Thr Cys Tyr
 610

1851

<210> 14
 <211> 612
 <212> PRT
 <213> Artificial Sequence

<400> 14
 Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
 1 5 10 15

Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
 20 25 30

Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
 35 40 45

Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
 50 55 60

Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
 65 70 75 80

Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
 85 90 95

Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
 100 105 110

Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
 115 120 125

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
 130 135 140

Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
 145 150 155 160

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
 165 170 175

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
 180 185 190

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
 195 200 205

Ser Pro Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Leu



210

215

220

Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser
225 230 235 240

Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
245 250 255

Glu Phe Ile Leu Ala Ala His Val Ala Glu Met Asn Pro Asn Val Asn
260 265 270

Val Phe Val Pro Pro Arg Asp Gly Phe Ser Gly Pro Ala Pro Arg Lys
275 280 285

Ser Lys Leu Ile Cys Glu Ala Thr Asn Phe Thr Pro Lys Pro Ile Thr
290 295 300

Val Ser Trp Leu Lys Asp Gly Lys Leu Val Glu Ser Gly Phe Thr Thr
305 310 315 320

Asp Pro Val Thr Ile Glu Asn Lys Gly Ser Thr Pro Gln Thr Tyr Lys
325 330 335

Val Ile Ser Thr Leu Thr Ile Ser Glu Ile Asp Trp Leu Asn Leu Asn
340 345 350

Val Tyr Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Leu Lys Asn
355 360 365

Val Ser Ser Thr Cys Ala Ala Ser Pro Ser Thr Asp Ile Leu Asn Phe
370 375 380

Thr Ile Pro Pro Ser Phe Ala Asp Ile Phe Leu Ser Lys Ser Ala Asn
385 390 395 400

Leu Thr Cys Leu Val Ser Asn Leu Ala Thr Tyr Glu Thr Leu Ser Ile
405 410 415

Ser Trp Ala Ser Gln Ser Gly Glu Pro Leu Glu Thr Lys Ile Lys Ile
420 425 430

Met Glu Ser His Pro Asn Gly Thr Phe Ser Ala Lys Gly Val Ala Ser
435 440 445

Val Cys Val Glu Asp Trp Asn Asn Arg Lys Glu Phe Val Cys Thr Val
450 455 460

Thr His Arg Asp Leu Pro Ser Pro Gln Lys Lys Phe Ile Ser Lys Pro
465 470 475 480

Asn Glu Val His Lys His Pro Pro Ala Val Tyr Leu Leu Pro Pro Ala
485 490 495

Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Val Thr Cys Leu Val
500 505 510

Lys Gly Phe Ser Pro Ala Asp Ile Ser Val Gln Trp Lys Gln Arg Gly



515

520

525

Gln Leu Leu Pro Gln Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu
530 535 540

Pro Gly Ala Pro Gly Phe Tyr Phe Thr His Ser Ile Leu Thr Val Thr
545 550 555 560

Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr Thr Cys Val Val Gly His
565 570 575

C
amended Glu Ala Leu Pro His Leu Val Thr Glu Arg Thr Val Asp Lys Ser Thr
580 585 590

Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Ile Met Ser Asp Thr Gly
595 600 605

Gly Thr Cys Tyr
610